

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/947,081A

Source: O I P E

Date Processed by STIC: 08/09/2001

COPY OF PAPERS
ORIGINALLY FILED

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/847,081A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☒ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/847,081A

TIME: 12:44:02

Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

3 <110> APPLICANT: BAYER AG
 5 <120> TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
 7 <130> FILE REFERENCE: Le A 34 326
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/847,081A
 C--> 10 <141> CURRENT FILING DATE: 2001-05-02
 12 <160> NUMBER OF SEQ ID NOS: 10
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1728
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Nicotiana tabacum
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (244)..(1566)
 25 <400> SEQUENCE: 1

26 agaaaccag aaagaacaac aggttttgct tcttggtgat gaggcattt gcctctgctt 60
 28 gtgtaaggca aagtcggttc actttcttat atccgatttt tataatcggt gaaattagtg 120
 30 gatagactct agtggatatac tacaagtatt gggtttttga taaaataggc tgaggtgaga 180
 32 aggttaacata aaggaaagac aaaaacttgg gaattgtttt agaccaccga gggttcttgt 240
 34 ttc atg agc atg tct gtt gct ttg ttg tgg gtt gtt tct ccc act tcc 288
 35 Met Ser Met Ser Val Ala Leu Leu Trp Val Val Ser Pro Thr Ser
 36 1 5 10 15
 38 gag gtc tcg aat ggg aca gga ttg ttg gat tca gtc cga gaa gga aac 336
 40 Glu Val Ser Asn Gly Thr Gly Leu Leu Asp Ser Val Arg Glu Gly Asn
 41 20 25 30
 43 cgc gtc ttt gta tca tcc agg ttc cta gct cga gat agg aat ttg atg 384
 45 Arg Val Phe Val Ser Ser Arg Phe Leu Ala Arg Asp Arg Asn Leu Met
 46 35 40 45
 48 tgg aat ggg aga atc aag aaa ggt ggg aga caa agg tgg aat ttt ggc 432
 50 Trp Asn Gly Arg Ile Lys Lys Gly Gly Arg Gln Arg Trp Asn Phe Gly
 51 50 55 60
 53 tct tta att gct gat cca aga tat tca tgc ttg ggt gga tca aga act 480
 56 Ser Leu Ile Ala Asp Pro Arg Tyr Ser Cys Leu Gly Gly Ser Arg Thr
 57 65 70 75
 59 gaa aag gga agc act ttc tct gta cag tcc agt ttg gtg gct agc cca 528
 61 Glu Lys Gly Ser Thr Phe Ser Val Gln Ser Ser Leu Val Ala Ser Pro
 62 80 85 90 95
 64 gct gga gaa atg act gtg tca tca gag aaa aag gtg tat gat gtg gta 576
 66 Ala Gly Glu Met Thr Val Ser Ser Glu Lys Lys Val Tyr Asp Val Val
 67 100 105 110
 69 tta aag cag gca gct tta gtg aag agg cag ctg aga tct acc gat gat 624
 71 Leu Lys Gln Ala Ala Leu Val Lys Arg Gln Leu Arg Ser Thr Asp Asp
 72 115 120 125
 74 tta gaa gtg aag ccg gat att gtt gtt cca ggg aat ttg ggc ttg ttg 672
 76 Leu Glu Val Lys Pro Asp Ile Val Val Pro Gly Asn Leu Gly Leu Leu
 77 130 135 140
 79 agt gaa gca tat gat cgt tgt ggc gaa gta tgt gca gag tat gca aag 720

Does Not Comply
 Corrected Diskette Needed

p. 4 Error

RAW SEQUENCE LISTING

DATE: 08/09/2001

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TIME: 12:44:02

Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

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81 Ser Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Ala Lys
82      145              150              155
84 aca ttt tac tta gga acc aag cta atg acc cca gag aga aga aga gct 768
86 Thr Phe Tyr Leu Gly Thr Lys Leu Met Thr Pro Glu Arg Arg Arg Ala
87 160              165              170              175
89 atc tgg gca ata tat gtg tgg tgc agg aga acg gat gag ctt gtt gat 816
91 Ile Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp
92              180              185              190
94 ggc cct aat gca tcc cac ata act ccg caa gct tta gat agg tgg gag 864
96 Gly Pro Asn Ala Ser His Ile Thr Pro Gln Ala Leu Asp Arg Trp Glu
97              195              200              205
99 acc agg ctg gaa gat att ttc agt ggg cgg cca ttt gat atg ctt gat 912
101 Thr Arg Leu Glu Asp Ile Phe Ser Gly Arg Pro Phe Asp Met Leu Asp
102              210              215              220
104 gct gct tta tcc gat act gtc tcc aga ttt cct gtt gat att cag cca 960
106 Ala Ala Leu Ser Asp Thr Val Ser Arg Phe Pro Val Asp Ile Gln Pro
107              225              230              235
109 ttc aga gat atg att gaa gga atg cgt atg gac ttg tgg aaa tcc aga 1008
111 Phe Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Trp Lys Ser Arg
112 240              245              250              255
114 tac aaa act ttc gat gag cta tat ctc tat tgt tac tat gtt gct ggt 1056
116 Tyr Lys Thr Phe Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly
117              260              265              270
119 act gta gga ttg atg agt gtt cca gtt atg ggt att gca cct gaa tca 1104
121 Thr Val Gly Leu Met Ser Val Pro Val Met Gly Ile Ala Pro Glu Ser
122              275              280              285
124 aag gca aca aca gag agt gta tat aat gct gct ttg gct tta ggg ctt 1152
126 Lys Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Leu
127              290              295              300
129 gca aat caa cta acc aat ata ctc aga gat gta gga gaa gat gcc aga 1200
131 Ala Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg
132              305              310              315
134 aga gga aga gta tac ttg cct caa gat gaa tta gca cag gca ggg ctc 1248
136 Arg Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu
137 320              325              330              335
139 tcc gac gaa gac ata ttt gct gga aga gtg act gat aag tgg agg aac 1296
141 Ser Asp Glu Asp Ile Phe Ala Gly Arg Val Thr Asp Lys Trp Arg Asn
142              340              345              350
144 ttt atg aag aaa caa att cag agg gcg agg aaa ttc ttt gat gag tca 1344
146 Phe Met Lys Lys Gln Ile Gln Arg Ala Arg Lys Phe Phe Asp Glu Ser
147              355              360              365
149 gag aaa ggt gtc aca gaa ctg gac tct gct agt aga tgg cct gtg tta 1392
151 Glu Lys Gly Val Thr Glu Leu Asp Ser Ala Ser Arg Trp Pro Val Leu
152              370              375              380
154 aca gcg ctg ctg ttg tat cgc aag ata ttg gac gag att gaa gcc aac 1440
156 Thr Ala Leu Leu Leu Tyr Arg Lys Ile Leu Asp Glu Ile Glu Ala Asn
157              385              390              395
159 gac tac aac aac ttc aca agg agg gct tat gtt agc aag cca aag aag 1488
161 Asp Tyr Asn Asn Phe Thr Arg Arg Ala Tyr Val Ser Lys Pro Lys Lys

```

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Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

```

162 400          405          410          415
164 ctt ctc acc ttg ccc att gct tat gca aaa tct ctt gtg ccc cct aat 1536
166 Leu Leu Thr Leu Pro Ile Ala Tyr Ala Lys Ser Leu Val Pro Pro Asn
167          420          425          430
169 aga act tcc tct cca cta gca aag aca tga atgaagtagt tgagtcaatg 1586
171 Arg Thr Ser Ser Pro Leu Ala Lys Thr
172          435          440
174 agtattatac actaaagaaa ctcagggtact tgtaaagtag atatatcttttg ctaaagtgtg 1646
176 atcatcaaaa gtagattgta aattcaatat gacaatctct tggtagaata ttttctccac 1706
178 actcatcaaa ccctcaagtg ag 1728
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 440
183 <212> TYPE: PRT
184 <213> ORGANISM: Nicotiana tabacum
186 <400> SEQUENCE: 2
187 Met Ser Met Ser Val Ala Leu Leu Trp Val Val Ser Pro Thr Ser Glu
188 1 5 10 15
190 Val Ser Asn Gly Thr Gly Leu Leu Asp Ser Val Arg Glu Gly Asn Arg
191 20 25 30
193 Val Phe Val Ser Ser Arg Phe Leu Ala Arg Asp Arg Asn Leu Met Trp
194 35 40 45
196 Asn Gly Arg Ile Lys Lys Gly Gly Arg Gln Arg Trp Asn Phe Gly Ser
197 50 55 60
199 Leu Ile Ala Asp Pro Arg Tyr Ser Cys Leu Gly Gly Ser Arg Thr Glu
200 65 70 75 80
202 Lys Gly Ser Thr Phe Ser Val Gln Ser Ser Leu Val Ala Ser Pro Ala
203 85 90 95
205 Gly Glu Met Thr Val Ser Ser Glu Lys Lys Val Tyr Asp Val Val Leu
206 100 105 110
208 Lys Gln Ala Ala Leu Val Lys Arg Gln Leu Arg Ser Thr Asp Asp Leu
209 115 120 125
211 Glu Val Lys Pro Asp Ile Val Val Pro Gly Asn Leu Gly Leu Leu Ser
212 130 135 140
214 Glu Ala Tyr Asp Arg Cys Gly Glu Val Cys Ala Glu Tyr Ala Lys Thr
215 145 150 155 160
217 Phe Tyr Leu Gly Thr Lys Leu Met Thr Pro Glu Arg Arg Arg Ala Ile
218 165 170 175
220 Trp Ala Ile Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp Gly
221 180 185 190
223 Pro Asn Ala Ser His Ile Thr Pro Gln Ala Leu Asp Arg Trp Glu Thr
224 195 200 205
226 Arg Leu Glu Asp Ile Phe Ser Gly Arg Pro Phe Asp Met Leu Asp Ala
227 210 215 220
229 Ala Leu Ser Asp Thr Val Ser Arg Phe Pro Val Asp Ile Gln Pro Phe
230 225 230 235 240
232 Arg Asp Met Ile Glu Gly Met Arg Met Asp Leu Trp Lys Ser Arg Tyr
233 245 250 255
235 Lys Thr Phe Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly Thr
236 260 265 270

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DATE: 08/09/2001

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Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

238 Val Gly Leu Met Ser Val Pro Val Met Gly Ile Ala Pro Glu Ser Lys
239 275 280 285
241 Ala Thr Thr Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Leu Ala
242 290 295 300
244 Asn Gln Leu Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg Arg
245 305 310 315 320
247 Gly Arg Val Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu Ser
248 325 330 335
250 Asp Glu Asp Ile Phe Ala Gly Arg Val Thr Asp Lys Trp Arg Asn Phe
251 340 345 350
253 Met Lys Lys Gln Ile Gln Arg Ala Arg Lys Phe Phe Asp Glu Ser Glu
254 355 360 365
256 Lys Gly Val Thr Glu Leu Asp Ser Ala Ser Arg Trp Pro Val Leu Thr
257 370 375 380
259 Ala Leu Leu Leu Tyr Arg Lys Ile Leu Asp Glu Ile Glu Ala Asn Asp
260 385 390 395 400
262 Tyr Asn Asn Phe Thr Arg Arg Ala Tyr Val Ser Lys Pro Lys Lys Leu
263 405 410 415
265 Leu Thr Leu Pro Ile Ala Tyr Ala Lys Ser Leu Val Pro Pro Asn Arg
266 420 425 430
268 Thr Ser Ser Pro Leu Ala Lys Thr
269 435 440
273 <210> SEQ ID NO: 3
274 <211> LENGTH: 1712
275 <212> TYPE: DNA
276 <213> ORGANISM: Nicotiana tabacum
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (333)..(1565)
282 <220> FEATURE:
W--> 283 <221> NAME/KEY: Xaa — noncritical Error should be unknown or unsure
284 <222> LOCATION: 135, 139 OK need to add location 51
285 <223> OTHER INFORMATION: Xaa is unknown or other OK
W--> 286 <400> SEQUENCE: 3
W--> 287 cttgaagagt agcagcagca agcaagahaa ttaaagtggg ctatttbkka naagccattg 60
289 ttacmagara attaagaagc caagamacag gttattttct acttgagtya ggaaaagttg 120
291 gtttgettta tttgtgggct ttttataatc ttttttccac aagggaaggt gggatttttc 180
293 ttgaaagtgg atttagactc tagtggaat ctactaggag taaatttatt aattttttat 240
295 aaattaagca gaggaaggaa ggaacagaa aacagaaagt aagacaaaaa accttgaat 300
297 tgttttagaa agccaaggtt ttcctgttca aa atg tct gtt gcc ttg tta tgg 353
298 Met Ser Val Ala Leu Leu Trp
299 1 5
301 gtt gtt tca cct tgt gaa gtc tca aat ggg aca gga ttc ttg gat tca 401
303 Val Val Ser Pro Cys Glu Val Ser Asn Gly Thr Gly Phe Leu Asp Ser
304 10 15 20
306 gtc cgg gag gga aac cgg gtt ttt gat tgc tgc agg cat agg aat tta 449
308 Val Arg Glu Gly Asn Arg Val Phe Asp Ser Ser Arg His Arg Asn Leu
309 25 30 35
311 gtg tgc aat gag aga aac aag aga ggt gtg aaa caa agg tgg aat ttt 497

Critical Error
n at location 51 is not
described.

RAW SEQUENCE LISTING

DATE: 08/09/2001

PATENT APPLICATION: US/09/847,081A

TIME: 12:44:02

Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

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313 Val Cys Asn Glu Arg Asn Lys Arg Gly Val Lys Gln Arg Trp Asn Phe
314 40 45 50 55
316 ggt tct gta agg tct gct atg gtg gct aca ccg gcg gga gaa atg gcg 545
318 Gly Ser Val Arg Ser Ala Met Val Ala Thr Pro Ala Gly Glu Met Ala
319 60 65 70
321 acg atg aca tca gaa cag atg gtt tat gat gtg gtt tta aaa caa gca 593
323 Thr Met Thr Ser Glu Gln Met Val Tyr Asp Val Val Leu Lys Gln Ala
324 75 80 85
326 gct tta gtg aag agg cag ttg aga tct gct gat gat tta gaa gtg aag 641
328 Ala Leu Val Lys Arg Gln Leu Arg Ser Ala Asp Asp Leu Glu Val Lys
329 90 95 100
331 ccg gag atc cct ctc ccc ggg aat ttg agc ttg ttg agt gaa gca tat 689
333 Pro Glu Ile Pro Leu Pro Gly Asn Leu Ser Leu Leu Ser Glu Ala Tyr
334 105 110 115
336 gat agg tgt agt gaa gta tgt gca gag tat gca aag aca ttt tac tth 737
W--> 338 Asp Arg Cys Ser Glu Val Cys Ala Glu Tyr Ala Lys Thr Phe Tyr Xaa
339 120 125 130 135
341 gga acc atg yta atg act cca gag aga aga agg gct att ttg gca ata 785
W--> 343 Gly Thr Met Xaa Met Thr Pro Glu Arg Arg Arg Ala Ile Trp Ala Ile
344 140 145 150
346 tat gtg tgg tgc agg aga aca gat gaa ctt gtt gat ggc cca aac gca 833
348 Tyr Val Trp Cys Arg Arg Thr Asp Glu Leu Val Asp Gly Pro Asn Ala
349 155 160 165
351 tca cat att aca ccc caa gcc tta gat agg tgg gaa gac cgg ctt gaa 881
353 Ser His Ile Thr Pro Gln Ala Leu Asp Arg Trp Glu Asp Arg Leu Glu
354 170 175 180
356 gat gtt ttc agc ggg cga cca ttt gat atg ctc gat gct gct ttg tcc 929
358 Asp Val Phe Ser Gly Arg Pro Phe Asp Met Leu Asp Ala Ala Leu Ser
359 185 190 195
361 gat act gtt tcc aag ttt cca gtt gat att cag ccg ttc aga gat atg 977
363 Asp Thr Val Ser Lys Phe Pro Val Asp Ile Gln Pro Phe Arg Asp Met
364 200 205 210 215
366 att gaa gga atg cgt atg gac ttg agg aag tca aga tat aga aac ttt 1025
368 Ile Glu Gly Met Arg Met Asp Leu Arg Lys Ser Arg Tyr Arg Asn Phe
369 220 225 230
371 gat gag ctt tac ctc tat tgt tat tac gtt gct ggt acg gtt ggg ttg 1073
373 Asp Glu Leu Tyr Leu Tyr Cys Tyr Tyr Val Ala Gly Thr Val Gly Leu
374 235 240 245
376 atg agt gtt cca att atg ggt att gca cct gat tca aag gca aca aca 1121
378 Met Ser Val Pro Ile Met Gly Ile Ala Pro Asp Ser Lys Ala Thr Thr
379 250 255 260
381 gag agc gta tat aat gca gct ttg gct tta gga atc gca aat caa cta 1169
383 Glu Ser Val Tyr Asn Ala Ala Leu Ala Leu Gly Ile Ala Asn Gln Leu
384 265 270 275
386 acg aac ata ctc aga gat gtt gga gaa gat gcc aga aga gga aga gtc 1217
388 Thr Asn Ile Leu Arg Asp Val Gly Glu Asp Ala Arg Arg Gly Arg Val
389 280 285 290 295
391 tac tta cct caa gat gaa tta gca cag gca ggt ctc ttc gac gat gac 1265
393 Tyr Leu Pro Gln Asp Glu Leu Ala Gln Ala Gly Leu Phe Asp Asp Asp

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/847,081A

DATE: 08/09/2001

TIME: 12:44:04

Input Set : A:\Mo6314 sequence-TEXT.txt

Output Set: N:\CRF3\08092001\I847081A.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:283 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:286 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:442 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:892 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5